1

SEQUENCE LISTING

<110> Itadani, Hiraku
      Takimura, Tetsuo
      Nakamura, Takao
      Kobayashi, Masahiko
      Tanaka, Ken-ichi
      Hidaka, Yusuke
      Ohta, Masataka

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)
      BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

<130> 06501-083001

<140> 09/891,053
<141> 2001-06-25

<150> PCT/JP99/07280
<151> 1999-12-24

<150> PCT/JP98/05967
<151> 1998-12-25

<150> JP 11/145661
<151> 1999-05-25

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 413
<212> PRT
<213> Rattus norvegicus

<400> 1
Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1   5   10   15
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
                20   25   30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
            35   40   45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
        50   55   60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65   70   75   80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
                85   90   95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
                100   105   110
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
            115   120   125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

```
            130                    135                    140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
145                    150                    155                    160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
                165                    170                    175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
                180                    185                    190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
                195                    200                    205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
            210                    215                    220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
225                    230                    235                    240
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
                245                    250                    255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
                260                    265                    270
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
                275                    280                    285
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
            290                    295                    300
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
305                    310                    315                    320
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
                325                    330                    335
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
                340                    345                    350
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
                355                    360                    365
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
            370                    375                    380
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
385                    390                    395                    400
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
                405                    410
```

<210> 2
<211> 1239
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)...(1239)

<400> 2

```
atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg      48
Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1               5                   10                  15


gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc      96
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
                20                  25                  30


tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca     144
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
                35                  40                  45
```

```
gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc          192
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
    50              55              60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac          240
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65              70              75              80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg          288
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
                85              90              95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg          336
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
            100             105             110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc          384
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
        115             120             125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc          432
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
    130             135             140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg          480
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
145             150             155             160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac          528
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
            165             170             175

ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc          576
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
            180             185             190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc          624
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
        195             200             205

acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac          672
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
    210             215             220

atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc          720
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
225             230             235             240

cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc          768
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
            245             250             255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg          816
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
            260             265             270
```

```
cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc        864
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
        275             280             285

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc        912
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
        290             295             300

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg        960
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
305             310             315             320

gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg       1008
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
                325             330             335

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc       1056
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
            340             345             350

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt       1104
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
            355             360             365

ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac       1152
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
        370             375             380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc       1200
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
385             390             395             400

aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag                   1239
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
            405             410
```

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 3
batngccaac ctbkccttct c   21

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature
<222> (1)...(20)
<223> n = A,T,C or G

<400> 4
ccataaaagn nggggttgac   20

<210> 5
<211> 2700
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (351)...(1589)

<221> misc_feature
<222> (1)...(2700)
<223> n = A,T,C or G

<400> 5
aattcggcac gagcgggcag atcgcggggc gcactcggtt gcgcgctgag ctagggtgc   60
accgacgcac cgcgggcggc tggagctcgg ctttgctctc gctgcagcag ccgcgccgcc   120
cgccccactc cgctcagatt ccgacaccag cccctctgg atcgccctcc tggactctag   180
cccgggctct tgctccgacc ccgcggacca tgctccgggc gccccccgga aaaccgggct   240
gggcgaagag ccggcaaaga ttaggctcac gagcgggggc cccacccggc cacccagctc   300
tccgcccgtg ccctgcccgg tgtccccgag ccgtgtgagc ctgctgggcc atg gag   356
                                                         Met Glu
                                                           1

cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga   404
Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
          5   10   15

gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc   452
Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
   20   25   30

gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg   500
Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
  35   40   45   50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc   548
Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
                55   60   65

acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc   596
Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
                70   75   80

gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc   644
Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
                85   90   95

```
cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac        692
Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
    100             105             110

tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat        740
Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
115             120             125             130

gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag        788
Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
            135             140             145

ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg        836
Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
                150             155             160

gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct        884
Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
            165             170             175

ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac        932
Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr
    180             185             190

aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc        980
Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro
195             200             205             210

ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag       1028
Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln
            215             220             225

agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa       1076
Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu
            230             235             240

ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc       1124
Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys
            245             250             255

tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc       1172
Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser
    260             265             270

tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc aaa agg       1220
Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg
275             280             285             290

ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc atg aag       1268
Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg Met Lys
            295             300             305

atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg gac aag       1316
Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg Asp Lys
            310             315             320

aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg ctc tgc       1364
```

```
        Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys
            325                 330                 335

        tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc cat ggc      1412
        Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys His Gly
            340                 345                 350

        cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt ctg tgg      1460
        Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp
        355                 360                 365                 370

        gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc      1508
        Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser
                        375                 380                 385

        ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc      1556
        Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val
                    390                 395                 400

        cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgagcagctg ccccaccctt    1609
        Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
                405                 410

        ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg gggccctggt    1669
        ccatgctccg ctccaaatgc catggcggcc tcttagatca tcaaccccgc agtggggtag    1729
        catggcaggt gggccaagag ccctagttgg tggagctaga gtgtgctggt tagctctgcc    1789
        gccacattct ccttcaccac acagaagaga caatccagga gtcccaggca tgccttccac    1849
        ctacacacac acacacacac acacacacac acaccacga gtgcagtgcc agtgatgtcc      1909
        ccttttgcat atttagtggt tggtgtcctc cctaatgcaa acctcggtgt gtgctcccgg    1969
        ctccggccct ggcaatgcgt gcgtgcgccc tgcatgtgct cacacccgcc acacacccgc    2029
        ccgccacaca cttgcaacac ctcctctctc ccagaagagc tggggacgat gccctttgct    2089
        gccactgtct cttgcttaat cccagagcct ggctccttat cccccactct cccttcaact    2149
        ctgccccaca aagtgtcgag cgcctcggga aacttgaagc ttctctgctc cttccactct    2209
        ggatgttttc aggaagatgg aggagaagaa aacacgtctg tgaacttgat gttccttgga    2269
        tgtttaatca agagagacaa aattgccgag gagctcgggg ctggattggc aggtgtgggc    2329
        tcccacgccc tcctccctca gtgctgcagc ttccggctga gccgcgccag ctgcttctgc    2389
        ctgccccgcc cccaggcttg ggacgatggc cctgccctgc ttgccccgtc tgtacaatca    2449
        gaatttgggg gtgggtggtt atggggtaga gcggctcttc actgtgccct aaaggtcctg    2509
        aggctcacag gacagtcagc aggagagcag gcaggcccgc gacacctggg aggaatgctt    2569
        tgcctcgtcc tgtgtactca cctcaggctt ctgcatgctc tgctgccctt gtgccctggt    2629
        gtgctgcctc tgccaatgtg aaaacacaat aaagtgtatt tttttacgga aaaaaaaana    2689
        aaaaaaaaaa a                                                         2700
```

```
<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 6
cgaggatccg tgaggctccg gtgcccgtc                                           29

<210> 7
<211> 32
<212> DNA
```

<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 7
cgggtaagct tcacgacacc tgaaatggaa ga   32

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 8
ccttctgcat cccattgtac gtacc   25

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 9
cttccgccgg gccttcacca a   21

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 10
acagacacgg cggggctcac   20

<210> 11
<211> 1350
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (280)...(557)

<221> misc_feature
<222> (1)...(1350)
<223> n = A,T,C or G

<400> 11
gcactcggct gcgcgttgcn tccggctgca cggtcgcacc ggcagcggct caggctccgg   60
ctcctctccc gctgcagcag ccgcgctgcc ggccccactg ggctcggatc cggccccggc   120

```
ccccctcggca  ccgcctgctc  tggccccggc  cccggccccg  cggaccatgc  gctgggcgcc      190
cccagggggaa  cccgacccgg  ccaagggccc  gcaaagacga  ggctcccggg  ccggggcccc      240
tcccggccgc  ccagctctcg  gccggcgccc  tgccccgcgt  cccggagccg  cgtgagcctg      300
cggggccatg  gagcgcgcgc  cgcccgacgg  gccgctgaac  gcttcggggg  cgctggcggg      360
cgaggcggcg  gcggcgggcg  gggcgcgcgg  cttctcggca  gcctggaccg  cggtgctggc      420
cgcgctcatg  gcgctgctca  tcgtggccac  ggtgctgggc  aacgcgctgg  tcatgctcgc      480
cttcgtggcc  gactcgagcc  tccgcaccca  gaacaacttc  ttcctgctca  acctcgccat      540
ctccgacttc  ctcgtcggta  aatccccagc  ccctggccgc  tggggaccca  ggggcgccca      600
gcgtggccgg  gccagcgggg  actggaacac  ggacctgggt  ggctcccgca  ggcacacgcc      660
ccaccagggg  acccggcctg  ggaagggggc  gtccggagcc  catggggtgg  ggggcacagg      720
cgaagttcct  tgccactcag  gcctcgggac  aggggctggg  gagagatgtc  cccgggaagg      780
gacacgggca  ctgggcgagg  cgcaaggcgc  aaaggcagcg  ggtgcagctc  tggctcctgc      840
gctgtagcca  aacaaaggct  gctgcggact  taggacgcgc  ggagggcgca  gtggggcggt      900
ttagagaagg  tctggggggag  gggacatgga  aggggggattt  ttagagctgt  gttgggggaa      960
gggacggtgg  ggaaggtggg  ggttgggggga  gacgctcgga  ggagcgtgct  ctcacgtgtc     1020
caggctctgc  tgccggctgg  ggggcggggc  acgcggaggg  ggctggagcg  ccagacacct     1080
gttgggggctg  tgaggtgcgt  ctcccagacg  ctccaagccc  gcttggcagt  agtagtagcg     1140
gctggcggct  ggcggctgca  accaagtgcc  ctttcagcca  ggagaaaggc  tttctccttg     1200
tctaagctga  gaccgagggt  tgtccagcgc  cagggtaggg  gctggagtcc  agcggggggag     1260
gggagaagga  aattgtcttc  tttcctcctt  tgagggctgg  gaggggctgga  cagaagtcca     1320
gggaatcccg  actccaggct  ctcggggggtc                                         1350
```

<210> 12
<211> 448
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (259)...(425)

<400> 12
```
gagctcccca  tgcctggatc  atccctcctg  cccccaggcc  caggggacac  agatagtgct       60
gggagctatg  tggggggtgaa  ggctggcggc  agggcagagt  ttgtggctga  caccaggtgg      120
aggggtggta  agatgaggat  ggctagttcc  agaaaagcag  ccaccatgtg  accccaggtc      180
ccgccggtgt  ctgcgcttag  gtccgtctgt  ccccctggccc  ctggctgcat  ggtcccactg      240
tggccctact  ccccacaggc  gccttctgca  tcccactgta  tgtaccctac  gtgctgacag      300
gccgctggac  cttcggccgg  ggcctctgca  agctgtggct  ggtagtggac  tacctgctgt      360
gcacctcctc  tgccttcaac  atcgtgctca  tcagctacga  ccgcttcctg  tcggtcaccc      420
gagcggtgag  tcctgggctg  cggagctc                                            448
```

<210> 13
<211> 1893
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (293)...(1209)

<400> 13
```
gagctcacag  ctggtagggg  gtggtaaaca  ggcagcctag  cagagagtga  gggttcaggt       60
tggtcccagg  gagcttctga  ggctctcact  gagtgtggca  gggcaccagt  ccgggacccc      120
agtgggggagg  gttagaggaa  gggagggggaa  agagggaggg  aggaggaca  ggagggggaaa      180
ggaggagcat  tgctgctgag  ggaagggccc  acatagggggc  ccacaggcta  cggggggcgca      240
cccagcccaa  tattccttcc  gccccgcccc  tgaccagcct  gcccttctgc  aggtctcata      300
ccgggcccag  cagggtgaca  cgcggcgggc  agtgcggaag  atgctgctgg  tgtgggtgct      360
```

```
ggccttcctg ctgtacggac cagccatcct gagctgggag tacctgtccg ggggcagctc      420
catccccgag ggccactgct atgccgagtt cttctacaac tggtacttcc tcatcacggc      480
ttccaccctg gagttcttta cgcccttcct cagcgtcacc ttctttaacc tcagcatcta      540
cctgaacatc cagaggcgca cccgcctccg gctggatggg gctcgagagg cagccggccc      600
cgagccccct cccgaggccc agccctcacc accccaccg cctggctgct ggggctgctg       660
gcagaagggg cacggggagg ccatgccgct gcacaggtat ggggtgggtg aggcggccgt      720
aggcgctgag gccggggagg cgaccctcgg gggtggcggt ggggcggct ccgtggcttc       780
acccacctcc agctccggca gctcctcgag gggcactgag aggccgcgct cactcaagag      840
gggctccaag ccatcggcgt cctcggcctc actggagaag cgcatgaaga tggtgtccca      900
gagcttcacc cagcgctttc ggctgtctcg ggacaggaaa gtggccaagt cgctggccgt      960
catcgtgagc atctttgggc tctgctgggc cccatacacg ctgctgatga tcatccgggc     1020
cgcctgccat ggccactgcg tccctgacta ctggtacgaa acctccttct ggctcctgtg     1080
ggccaactcg gctgtcaacc ctgtcctcta ccctctgtgc caccacagct ccgccgggc      1140
cttcaccaag ctgctctgcc cccagaagct caaaatccag ccccacagct ccctggagca     1200
ctgctggaag tgagtggccc accagagcct ccctcagcca cgcctctctc agcccaggtc     1260
tcctgggcat ctggccctgc tgcccctac ccggctcgtt cccccagggg tgagccccgc      1320
cgtgtctgtg gccctctctt aatgccacgg cagccaccct gccatggagg cgccttcctg     1380
ggttggccag agggcccctc actggctgga ctggaggctg ggtggccggc cctgcccccc     1440
acattctggc tccaccggga gggacagtct ggaggtccca gacatgctgc ccaccccctg     1500
ctggtgccca cccttcgcag ttactggttg gtgttcttcc caaagcaagc acctgggtgt     1560
gctccaggct tcctgcccta gcagtttgcc tctgcacgtg cacacacctg cacacccctg     1620
cacacacctg cacaccgtcc ctctcccCgg acaagcccag gacactgcct ttgctgcctt     1680
ctgtctcttg cataagcctc aggcctggcc ctttcacccc tcttcccacc aactctctct     1740
gcccccaaaa gtgtcaaggg gccctaggaa cctcgaagct gttctctgct tttccattct     1800
gggtgttttc agaaagatga agaagaaaac atgtctgtga acttgatgtt cctgggatgt     1860
ttaatcaaga gagacaaaat tgctgaggag ctc                                  1893
```

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 14
tgaacgcttc gggggcgctg   20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 15
gagatggcga ggttgagcag g   21

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 16
ggctccaagc catcggcgtc   20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 17
ctcacttcca gcagtgctcc   20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 18
gcctccgcac ccagaacaac   20

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 19
tgcgcctctg gatgttcag   19

<210> 20
<211> 453
<212> PRT
<213> Homo sapiens

<400> 20
Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu
1   5   10   15
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
            20   25   30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
        35   40   45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
    50   55   60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65   70   75   80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
                85   90   95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
            100   105   110
Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

```
            115                    120                    125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
        130                    135                    140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp
145                    150                    155                    160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
                165                    170                    175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
                180                    185                    190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
                195                    200                    205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
        210                    215                    220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala
225                    230                    235                    240
Gly Pro Glu Pro Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro Pro
                245                    250                    255
Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu
                260                    265                    270
His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu
                275                    280                    285
Ala Thr Leu Gly Gly Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr
        290                    295                    300
Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
305                    310                    315                    320
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
                325                    330                    335
Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg
                340                    345                    350
Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly
                355                    360                    365
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
        370                    375                    380
His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
385                    390                    395                    400
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
                405                    410                    415
His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
                420                    425                    430
Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys
                435                    440                    445
Lys Lys Thr Cys Leu
                450
```

<210> 21
<211> 2050
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (271)...(1629)

<400> 21
agagatgtag ggcgcccctt ttagctgcgc acagaacgaa agaactcgtt ttttctttaa   60
gtgagtgtgc ttgggtgacg cttagggcgc cctccgcagt gcgcgcagga aagcgcactg   120
aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctccg tcgcggagtc   180

13

```
gctgagtccg tgccctttta gttagttctg cagtctagta tggtccccat ttgcccttcc     240
actcccggag ccgcgtgagc ctgcggggcc atg gag cgc gcg ccg ccc gac ggg     294
                                    Met Glu Arg Ala Pro Pro Asp Gly
                                     1                   5

ccg ctg aac gct tcg ggg gcg ctg gcg ggc gag gcg gcg gcg gcg ggc     342
Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly
        10              15              20

ggg gcg cgc ggc ttc tcg gca gcc tgg acc gcg gtg ctg gcc gcg ctc     390
Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu
25              30              35                      40

atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg     438
Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met
                45              50              55

ctc gcc ttc gtg gcc gac tcg agc ctc cgc acc cag aac aac ttc ttc     486
Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe
            60              65              70

ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc     534
Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile
            75              80              85

cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgg     582
Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg
        90              95              100

ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc     630
Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser
105             110             115                     120

tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg tcg gtc     678
Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val
                125             130             135

acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca     726
Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala
            140             145             150

gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga     774
Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly
        155             160             165

cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc     822
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro
        170             175             180

gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc     870
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile
185             190             195                     200

acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc     918
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe
                205             210             215
```

```
ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg       966
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg
            220             225             230

ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc      1014
Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Pro Glu Ala
            235             240             245

cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag      1062
Gln Pro Ser Pro Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys
            250             255             260

ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg      1110
Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala
265             270             275             280

gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg      1158
Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly Gly
            285             290             295

ggc ggc tcc gtg gct tca ccc acc tcc agc tcc ggc agc tcc tcg agg      1206
Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg
            300             305             310

ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg      1254
Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala
            315             320             325

tcc tcg gcc tcg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc      1302
Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe
            330             335             340

acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg      1350
Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu
345             350             355             360

gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg      1398
Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu
            365             370             375

ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac      1446
Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr
            380             385             390

tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac      1494
Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn
            395             400             405

cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc      1542
Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr
            410             415             420

aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg      1590
Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu
425             430             435             440

gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat      1639
Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu
```

```
Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu
              445                 450
```

```
gttcctggga tgtttaatca agagagacaa aattgctgag gagctcaggg ctggattggc    1699
aggtgtgggc tcccacgccc tcctccctcc gctaaggctt ccggctgagc tgtgccagct    1759
gcttctgccc accccgcctc tgggctcaca ccagccctgg tggccaagcc tgccccggcc    1819
actctgtttg ctcacccagg acctctgggg gttgttggga ggaggggggcc cggctgggcc    1879
cgagggtccc aaggcgtgca ggggcggtcc agaggaggtg cccgggcagg ggccgcttcg    1939
ccatgtgctg tgcacccgtg ccacgcgctc tgcatgctcc tctgcctgtg cccgctgcgc    1999
tgccctgcaa accgtgaggt cacaataaag tgtattttt tattggtgct g              2050
```

```
<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature
<222> (1)...(20)
<223> n = A,T,C or G

<400> 22
tgcatcccat tgtacgtncc                                                     20


<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature
<222> (1)...(20)
<223> n = A,T,C or G

<400> 23
atcattagga gcgtgtangg                                                     20


<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 24
tgctctggga caccatcttc                                                     20


<210> 25
<211> 445
<212> PRT
<213> Rattus norvegicus
```

<400> 25

```
Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
1               5                   10                  15
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
            20                  25                  30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
        35                  40                  45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
        50                  55                  60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65              70                  75                  80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
                85                  90                  95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
            100                 105                 110
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
            115                 120                 125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
    130                 135                 140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
145                 150                 155                 160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
                165                 170                 175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
            180                 185                 190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
        195                 200                 205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
    210                 215                 220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
225                 230                 235                 240
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
                245                 250                 255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
            260                 265                 270
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu
        275                 280                 285
Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr
    290                 295                 300
Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
305                 310                 315                 320
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ala Ser Leu Glu Lys Arg
            325                 330                 335
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
            340                 345                 350
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
        355                 360             .   365
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
    370                 375                 380
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
385                 390                 395                 400
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
            405                 410                 415
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
            420                 425                 430
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
            435                 440                 445
```

```
<210> 26
<211> 1953
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (302)...(1636)

<400> 26
agctaggggt gcaccgacgc accgcggcgg ctggagctcg gctttgctct cgctgcagca      60
gccgcgccgc ccgccccact ccgctcagat tccgacacca gccccctctg gatcgccctc     120
ctggactcta gccgggctc ttgctccgac cccgcggacc atgctccggg cgccccccgg      180
aaaaccgggc tgggcgaaga gccggcaaag attaggctca cgagcggggg ccccacccgg     240
ccacccagct ctccgcccgt gccctgcccg gtgtccccga gccgtgtgag cctgctgggc     300
c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg     349
  Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
   1               5                  10                  15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc     397
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
             20                  25                  30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca     445
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
         35                  40                  45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc     493
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
     50                  55                  60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac     541
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65                  70                  75                  80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg     589
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
                 85                  90                  95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg     637
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
                100                 105                 110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc     685
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
             115                 120                 125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc     733
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
         130                 135                 140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg     781
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
145                 150                 155                 160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac     829
```

```
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
                165                 170                 175

ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc       877
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
            180                 185                 190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc       925
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
            195                 200                 205

acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac       973
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
        210                 215                 220

atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc      1021
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
225                 230                 235                 240

cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc      1069
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
                245                 250                 255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg      1117
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
            260                 265                 270

cac agg tat ggg gtg ggt gag gca ggc cct ggt gtt gag gct ggg gag      1165
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu
            275                 280                 285

gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tcg ccc acc      1213
Ala Ala Leu Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Ser Pro Thr
        290                 295                 300

tcc agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc      1261
Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
305                 310                 315                 320

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc      1309
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
                325                 330                 335

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg      1357
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
            340                 345                 350

gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg      1405
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
            355                 360                 365

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc      1453
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
            370                 375                 380

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt      1501
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
```

```
     385                    390                    395                    400

ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac        1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
                405                    410                    415


tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc        1597
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
                420                    425                    430


aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgagcagctg        1646
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
            435                    440                    445


ccccaccctt ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcgtgggcg     1706
gggccctggt ccatgctccg ctccaaatgc catggcggcc tcttagatca tcaaccccgc     1766
agtggggtag catggcaggt gggccaagag ccctagttgg tggagctaga gtgtgctggt     1826
tagctctgcc gcacattctc cttcaccaca cagaagagac aatccaggag tcccaggcat     1886
gccttcacct acacacacac acacacac acacacac acaccacagt gcagtgccag          1946
tgatgtc                                                                1953
```